

SEQUENCE LISTING

<110> AMRAD Operations Pty Ltd

<120> A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
FAMILY OF APOPTOSIS-CONTROLLING GENES

<130> 11686a

<150> 09/155,327

<151> 1997-03-27

<150> PN8965

<151> 1996-03-27

<160> 9

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Mouse

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Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
      20             25             30

ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca   144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
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gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg   192
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      50             55             60

gcg gct cag ctg cat gtg acc cca ggc tca gcc cag caa cgc ttc acc   240
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Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
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gta gcc ttc ttt gtc ttt ggg gct gca ctg tgt gct gag agt gtc aac   336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
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aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc   384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
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 165 170 175

gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576  
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Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu

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90

95

Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn

100

105

110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala

115

120

125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp

130

135

140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg

145

150

155

160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly

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175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser

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185

190

Lys

<210> 8

<211> 582

<212> DNA

<213> Mouse

<220>

<221> CDS

<222> (1)..(579)

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15

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Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
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Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
gct gga gac gag ttt gag acc cgt ttc cgc cgc acc ttc tct gac ctg	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
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Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
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cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
aaa gaa atg gag cct ttg gtg gga caa gtg cag gat tgg atg gtg gcc	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala	
115 120 125	
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Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
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Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg	
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cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg	528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly	
165 170 175	

gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576  
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
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aag tga 582  
 Lys

<210> 9  
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 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
 35 40 45  
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
 50 55 60  
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80  
 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
 85 90 95  
 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
 100 105 110  
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala  
 115 120 125  
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
 130 135 140  
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
 145 150 155 160  
 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
 165 170 175  
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190  
 Lys